

Applicant(s): Vimla Band

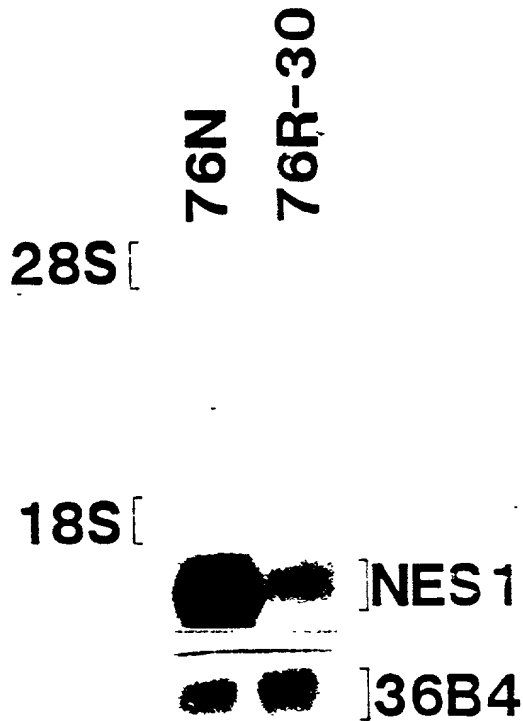
NES-1 POLYPEPTIDES, DNA, AND RELATED MOLECULES  
AND METHODS

FIG. 1

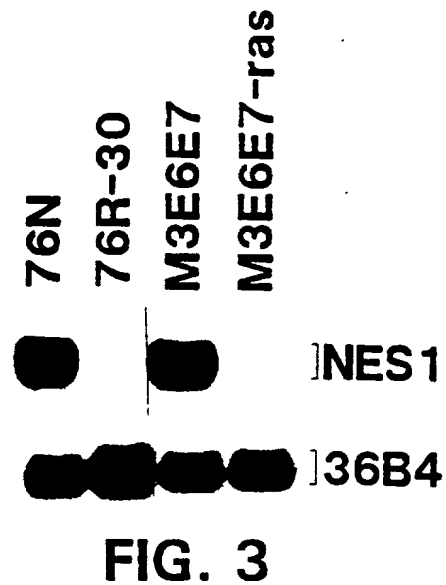


FIG. 3

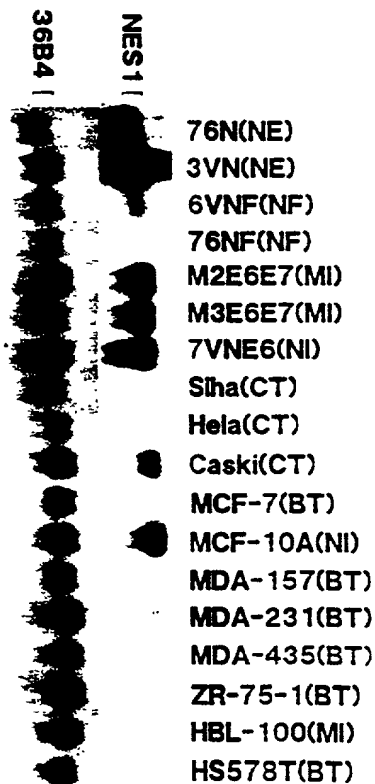


FIG. 2A

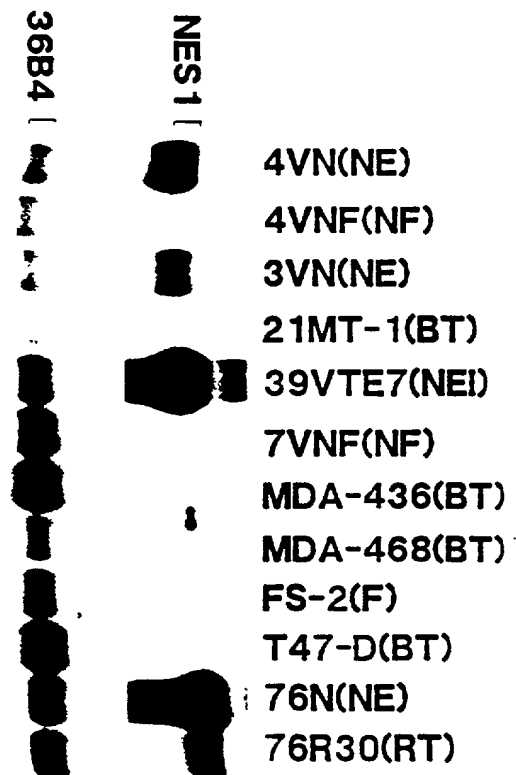


FIG. 2B

10021368.1.2120.1

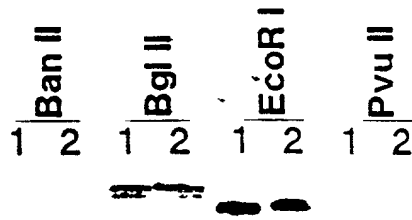


FIG. 4

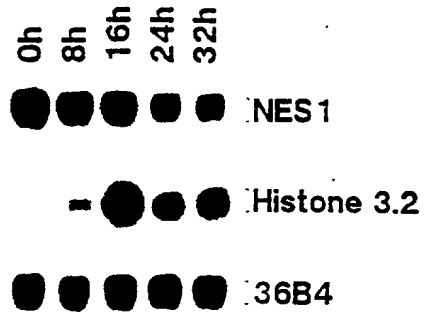


FIG. 5A



FIG. 6

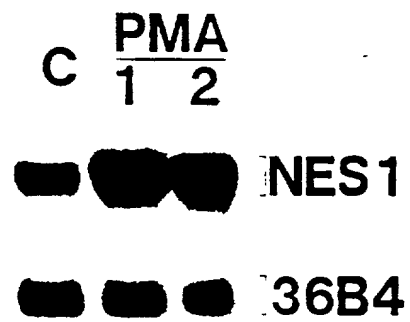
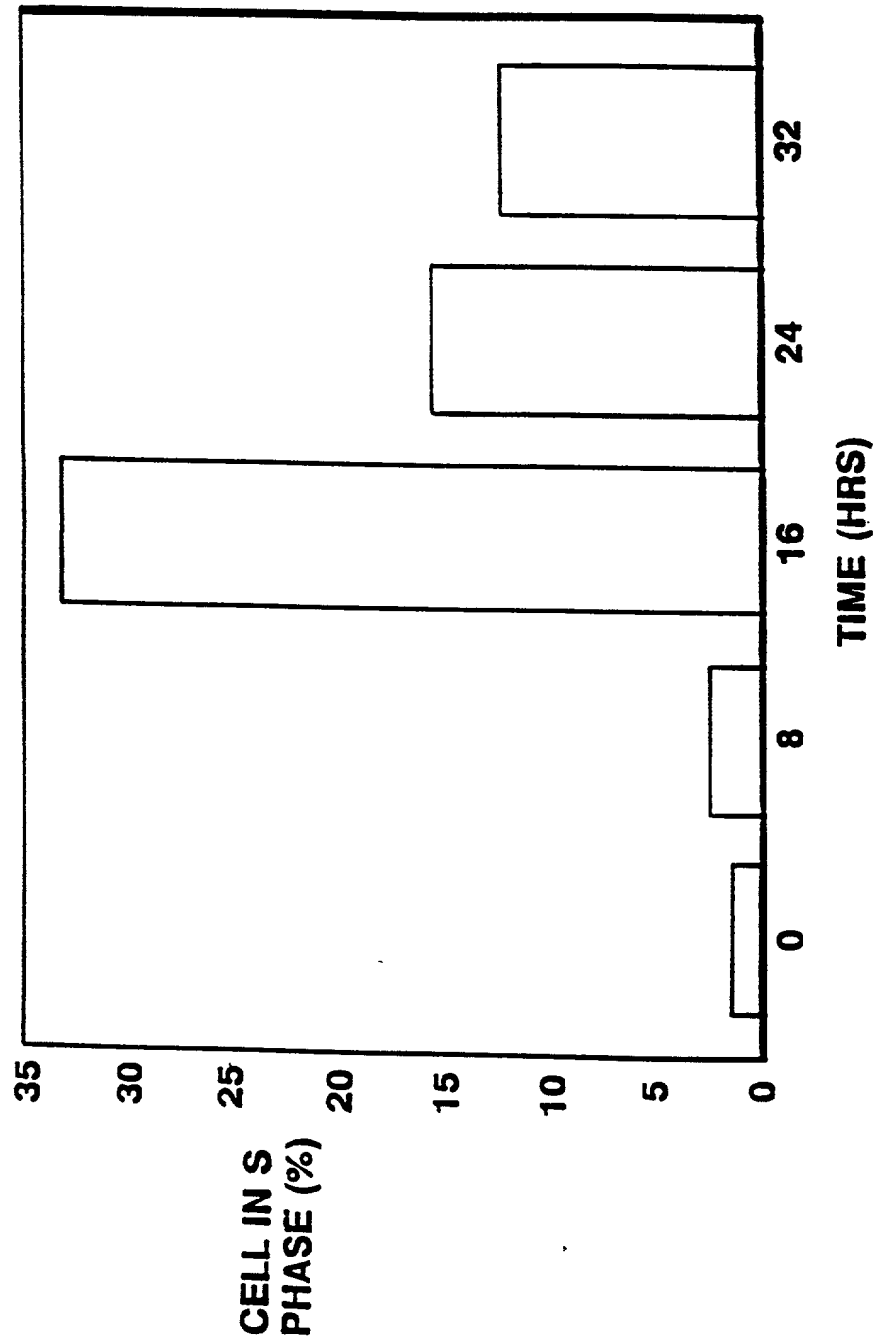


FIG. 8

FIG. 4

Applicant(s): Vimla Band

NES-1 POLYPEPTIDES, DNA, AND RELATED MOLECULES  
AND METHODS**FIG. 5B**

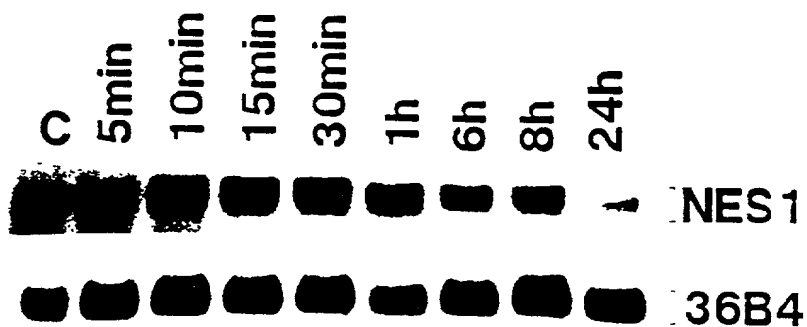


FIG. 7A

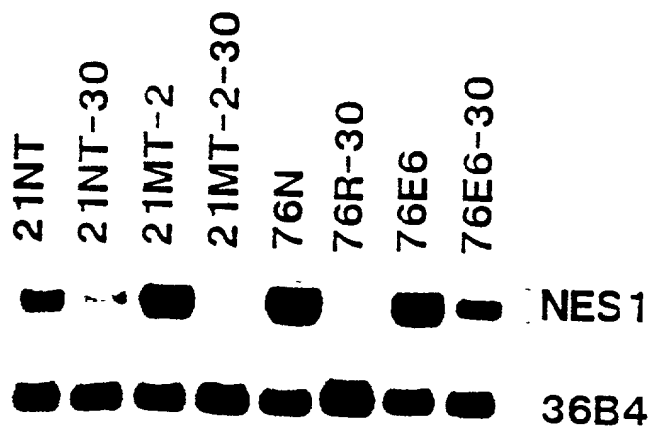


FIG. 7B

## Comparison of Sequences near putative active site

	86	137	223	224	227	228	229	230	231	241	243	245
NES 1	H	D	D	P	S	D	S	G	G	G	L	W
Human Pancreatic Trypsinogen III	H	D	D	S	R	D	S	G	G	G	V	W
	▲	▲	△	△			▲			△	△	△

▲: Catalytic triad

△: Residues important for substrate binding and specificity

FIG. 9A

## Alignment of NES 1 amino acid sequence with other serine proteases

	1				50
Mmtryar	..MSALLILA	LVGA.....	.....	AVAFPVDD.D	DKIVG...GY
Hstryivb	....LELHP	LLGGRTWRAA	RDADGCEALG	TVAVPFDD.D	DKIVG...GY
Rntrypvb	..MKICIFFT	LLGT.....	.....	VAAFPTEEDND	DRIVG...GY
Sstrypii	.....	.....	.....	.AAAFATE..D	DKIVG...GY
Nes1	MRAPHLHLSA	ASGARALAKL	LPLLMAQLWA	AEAALLPQND	TRLDPEAYGA
	51				100
Mmtryar	TCRESSVPYQ	VSLNAGYHF.	CGGSLINDQW	VVSAAHCYKY	RIQVRLGEHN
Hstryivb	TC.ENSILPYQ	VSLNSGSHF.	CGGSLISEQW	VVSAAHCYKT	RIQVRLGEHN
Rntrypvb	TCQEHSPYQ	VSLNAGSHI.	CGGSLITDQW	VLSAAHCYHP	QLQVRLGEHN
Sstrypii	ECKAYSQPHQ	VSLNSGYHF.	CGGSLVNENW	VVSAAHCYQS	RVEVRLGEHN
Nes1	PCARGSQPWQ	VSLFNGLSFH	CAGVLVDQSW	VLTAHCGNK	PLWARVGDH
	101				150
Mmtryar	INVLEGNEQF	VDSAKIIRHP	NYN.....	.SWTLDNDIM	LIKLASPVTL
Hstryivb	IKVLEGNEQF	INAAKIIRHP	KYN.....	.RDTLDNDIM	LIKLSPPAVI
Rntrypvb	IYEIEGAEQF	IDAAKMILHP	DYD.....	.KWTVDNDIM	LIKLSKSPATL
Sstrypii	IQVTEGSEQF	ISSSRVIRHP	NYS.....	.SYNIDNDIM	LIKLSKSPATL
Nes1	LLLLQG.EQL	RRTTRSVVHP	KYHGGSGPIL	PRRTDEHDL	LLKLARPVVP
	151		EXTRA INSERT		200
Mmtryar	NARVASVPLP	SSCAPAGTQC	LISGWGNTLS	NGVNNPDLLQ	CVDAFVLPQA
Hstryivb	NARVSTISLP	TAPPAAGTEC	LISGWGNTLS	FGADYPDELK	CLDAPVLTQA
Rntrypvb	NSKVSTIPLP	QYCPTAGTEC	LVSGWG.VLK	FGFESPSVLQ	CLDAPVLSDS
Sstrypii	NTYVQPVALP	TSCAPAGTMC	TVSGWGNTMS	STAD.KNKLQ	CLNIPILSYS
Nes1	GPRVRALQLP	YRCAQPGDQC	QVAGWGTTAA	RRVKYNKGLT	CSSITILSPK
	201				250
Mmtryar	DCEASYPGDI	TNNMICVGFL	EGGKDSCQGD	SGGPVVCNGE	LQGVVSWG.Y
Hstryivb	ECKASYPGKI	TNSMFCVGFL	EGGKDSCQRD	SGGPVVCNGQ	LQGVVSWG.H
Rntrypvb	VCHKAYPRQI	TNNMFCLGFL	EGGKDSCQYD	SGGPVVCNGE	VQGVVSWG.D
Sstrypii	DCNNSYPGMI	TNAMFCAGYL	EGGKDSCQGD	SGGPVVCNGE	LQGVVSWG.Y
Nes1	ECEVFYPGVV	TNNMICAG.L	DRGQDPCQSD	SGGPLVCDDET	LQGILSWGVY
	251				280
Mmtryar	GCAQPDAPGV	YTKVCNYVDW	IQNTIADN*.		
Hstryivb	GCAWKNRPGV	YTKVYNYVDW	IKDTIAANS*		
Rntrypvb	GCALEGKPGV	YTKVCNYLW	IQQTVAAN*.		
Sstrypii	GCAEPGNPGV	YAKVCIFNDW	LTSTMATY*.		
Nes1	PCGSAQHPAV	YTOICKYMSW	INKVIRSN*.		

FIG. 9B

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1 MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA  
51 PCARGSQPWQ VSLFNGLSFH CAGVLVDQSW VLTAAHCGNK PLWARVGDDH  
101 LLLLQGEQLR RTTRSVVHPK YHQGGPILP RRTDEHDIML LKLARPVVPG  
151 PRVRALQLPY RCAQPGDQCQ VAGWGTTAAR RVKYNKGITC SSITILSPKE  
201 CEVFYPGVVT NNMICAGLDR GQDPCQSDSG GPLVCDETLQ GILSWGVPYC  
251 GSAQHPAVYT QICKYMSWIN KVIRSN\* (SEQ ID NO: 1)

**FIG. 10**

1 ACCAGCGGCA GACCACAGGC AGGGCAGAGG CACGTCTGGG TCCCCTCCCT  
51 CATTCTATC GCGACTCCC AGATCCTGGC CATGAGAGCT CCGCACCTCC  
101 ACCTCTCCGC CGCCTCTGGC GCGCGGGCTC TGGCGAAGCT GCTGCCGCTG  
151 CTGATGGCGC AACTCTGGGC CGCAGAGGCG GCGCTGCTCC CCCAAAACGA  
201 CAGCGGCTTG GACCCCGAAG CCTATGGCGC CCCGTGCGCG CGCGGCTCGC  
251 AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT  
301 GTCCTGGTGG ACCAGAGTTG GGTGCTGACG GCGCGGCACT GCGGAAACAA  
351 GCCACTGTGG GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG  
401 AGCAGCTCCG CCGGACGACT CGCTCTGTTG TCCATCCCAA GTACCACCAG  
451 GGCTCAGGCC CCATCCTGCC AAGGCGAACG GATGAGCAGG ATCTCATGTT  
501 GCTAAAGCTG GCCAGGCCCC TAGTGCCGGG GCGCGCGCTC CCGGCCCTGC  
551 AGCTTCCCTA CCGCTGTGCT CAGCCCCGAG ACCAGTGCCA GGTGCTGGC  
601 TGGGGCACCA CGGCCGCCCC GAGAGTGAAG TACAACAAGG GCCTGACCTG  
651 CTCCAGCATC ACTATCCTGA GCCCTAAAGA GTGTGAGGTC TTCTACCCTG  
701 GCGTGGTCAC CAACAACATG ATATGTGCTG GACTGGACCG GGGCCAGGAC  
751 CCTTGCCAGA GTGACTCTGG AGGCCCCCTG GTCTGTGACG AGACCCTCCA  
801 AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC CAGCATCCAG  
851 CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA  
901 CGCTCCAAC TATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT  
951 CCTGCTGATC CAGATGCCCC GAGGCTCCAT CGTCCATCCT CTTCCTCCCC  
1001 AGTGGGCTGA ACTCTCCCC TGTCTGCACT GTTCAAACCT CTGCCGCCCT  
1051 CCACACCTCT AAACATCTCC CCTCTCACCT CATTCCCCCA CCTATCCCCA  
1101 TTCTCTGCCT GTACTGAAGC TGAAATGCAG GAAGTGGTGG CAAAGGTTTA  
1151 TTCCAGAGAA GCCAGGAAGC CGGTCATCAC CCAGCCTCTG AGAGCAGTTA  
1201 CTGGGGTCAC CCAACCTGAC TTCCTCTGCC ACTCCCCGCT GTGTGACTTT  
1251 GGGCAAGCCA AGTGCCCTCT CTGAACCTCA GTTTCCTCAT CTGCAAAATG  
1301 GGAACAATGA CGTGCCTACC TCTTAGACAT GTTGTGAGGA GACTATGATA  
1351 TAACATGTGT ATGTAAATCT TCATGTGATT GTCATGTAAG GCTTAACACA  
1401 GTGGGTGGTG AGTTCTGACT AAAGGTTACC TGTGTGCTG AAAAAAAAAA  
1451 AAAA (SEQ ID NO: 2)

FIG. 11